

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCCGCCGGCTGGGCTCCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA
GGCGACGGGTCCGCCGGTGCACATGGGTACCAAGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATTCGACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCAAGAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCACACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGACTTACCCCTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATAACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAAGGGCGGCCGCACTTGTGTTATTGCAGCTTAAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTTCACTGCATTCTAGTTGTGGTTGTCAAAC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATCGGCGCAGCACCATGGCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGAC CCTCGG TTCTAT CGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCAC CGCGTCCGCCAGGCCGGAGGCGACGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGC
GGGCCGCCGCAGGAGGAGCCTGTACCTATGGATCGATGCTACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAAGGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACCTCTATGAATTCCCTGTGCCTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGCCCTGCTGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCTTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAAGCTGAGTGCCAGGCGGGTGCAGAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGACTTGTGTGACTCCCTGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGACAAGCAAACGCTCAACCACCTGCTTAAATGGAGGACC
TGTTCTACCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCAACCTGCGAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGGTGCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAAGGCCAGGAGCAGGCCAGCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCAAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTCTGTTCACTGCTTGGACAGATTTATATTATGTCAATTGA
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTTCAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAACATCAGAAAGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTTATTGTCAAGATATTAGAT
GTTTGTACATTTAAAATTGCTCTTAAATTAACTCTCAATACAATATATTGACC
TTACCATATTCCAGAGATTCACTGATTAAAAAAATTACAATGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACCTTGCAT
TGGCTTGAAGCAATATAATATATTGTAACAAAACACAGCTCTTACCTAATAAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTGGAAAAAA
AAAAAAAAAAAAAAAAAAGGCCGGCCGCACTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTATTGCAGCTTATAATG

FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPFCICPPGFYGVNCDKANCST
TCFNNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGTGCAGAGCCAGGAGGCGGAGGCAGCGCGGGCCAGCCTGGG
CCCCAGCCCCACACCTTACCAAGGGCCAGGAGCCACC**ATGTGGCGATGTCCACTGGGGCTAC**
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGTGCCTGGGAGGGCGGTACTGCCAGGA
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGGACGCCGGAGGGCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCCGTGCCGACGACTGTGCCCTGCCACTCTGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCCACGGTCTCCGACTGCTGCCCTGACTCTGGGACTTC
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGTATCTA
TCCAGTCTTGGAACGTACTGGGACAACGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGAACTATGGCTGGCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCGTGG**ATGA**GGGCATTGCTACCGCTGGCACCA
TCCGCCATCTCCTCGGTATGAAACATGCATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAAACCTGATTATGAGCCTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCTGTCGCCAGAACCTGCTGTCTTGAC
ACCCACCAAGCAGCAGGGCTGCCGCCGTCTCGATGGTGCCTGGTGGTCTGCC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGCC
CTGCCGCCCTGTATGATGCACAGCCAGGCATGGTGGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCTCA
TGGAGGTGCATGAGGAACCTCTTCTTACAAAGGGAGGCATCTACAGCCACAGCCAGTGGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGCGCCGGCTCAATGAGTGCACATCGAG
AGCTTCTGCTGGCGTCTGGGCGTGGGATCCAGGCTAAGGGCCGGGAAGAGGCCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGGCGCAGGCCGCCAGGGCGCTAAT
CCCGCGCGGGTCTCGCTGACGAGCGCCCTGGAGCCGCCAGGCAGACTGGCG
GAGCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGCCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCAATACCCACCCCAATCCGTATTCTTTTTTTAGACAGGGCTTGCTCC
TTGCCCAAGGTGGAGTGCACTGGCCATCAGGGCTACTGTAACCTCGACTCCTGGGTTCA
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGAAAGAGGGGGCTCACTGTGTTGCCAGGCTGGTTTCGAAC
CCTGGGCTCAAGGGTCCACCTGCCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTACAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTGCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCCTGCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTGGCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAAGTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGGCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPASFSTLNPLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCCGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGGAAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCGGCAGGGGCCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCAGGCCACTTCATCAAGCGCCTTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACAGCAGTCAGTTGAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGGCCGCCTCCC
CACCCCTTCCCTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGCCGGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTCCCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCAACGCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDVFTEIVLE
NNYTAFQONARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTCTTCCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCAAACCTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCAGACAGGAACTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTAACCTCCACAACAACAAATTAAATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAACATGTCAGAGTTCTCCATTGCAGGAAAAC
AAATATTCAAGACCATTTCACGGGCTGCTCTGCCAGCTCTGAAGAGCTGACACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACATCACCTGAGCAGTGTGCCTGTTGGCTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAACGTAATTGCTGTCC
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAGAT
AAACACATTCCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTGATAATCTCTCCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGTGACTGCAGTATTAATGGGTACAGAACATGGCTCAA
ATATATCCCTCATCTCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCGTCAGGAAATTAAATATGAATCTTGTCCCTGTCCCACGACCCCCGGCCTG
CCTCTCTTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAACGCTACACGCCTCCAACCTTACCAACATCGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTCTATC
CATTGTAATGATACTCCATTCAAGTCAGCTGGCTCTCTTCAACGTGATGGCATA
CAAACTCACATGGGTAAAATGGGCACAGTTAGTAGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAACACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTGTTAGTGCCACTGGATGCTTTAACCTACCGCGCGGTAGAAGACACCATTGTTAGAGGC
CACCACCCATGCCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGCCTAGCGTCTTGTGGCATATGCACAAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACACCGGGCGGCCGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAAGATCGTCTCCTTAAATAACGAT
CAAACCTTAAAGGAGATTCAAGACTGCAGCCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACATGCCGATACTGCAACAGCAGCGTCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGCACATAAGAACACGCAGATTACATTGATAATGGGATTTAAAAAGTG
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTTAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNVQSVHTVLYGNQLDEFPMNLPKNVRLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNMNLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDRERVTTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGMHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTCSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNNDQLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGGCGGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCCTGCCCTCCACGAGCG
ATCCCCGAGGAGAGCCCGGGCCCTCGGCAGGGCAAGAGGCCAGGAGGAAGACCCGGTGGCTGCGCCCTGCC
TCGCTTCCCAGGGCCGGCGGCTGCAGGCTTGCCTGCCCTTGTGCTGCCCTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGGACAGATCGTCCCTCCCTGCCAGGGCAGGGAGCGGTACGTGGGAGGGTCCATCT
CTAGGGGAGACACGCTCGGACCCACCCGAGACGGGCTTCTGGAGAGTTCTGTGAGAACAAGCAGGGCAGACC
TGGTTTCATCATGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATGTGGACA
TCTTGCATTGGACATTGGCCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCAGTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCAGGGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTAGAAGCAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGATCCTAATCTTGCATTGGTGTGGGCCAGGTAGACTTCAAACACCTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTGTGGCCAATTCAAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCCACATGTGACGGCATAACTGTGCCACTCTGCATCAACATCCCTG
GTCATACGTCTGAGGTGCAAACAAGGCTACATTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGAATGTGCCGGCTCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTAATGTGCCCTCAGAAAACACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGCCTGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTCACAAGGATCAACTACTGTGACTGAAACAAACGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGGCT
ACTACTGCCGCTGCCACCGTGGTACACTTGACCCCAATGGCAAACACCTGCAGCCAGTGGGACACTGTGAC
AGCAGGACCATGGCTGTGAGCAGCTGTGAACACGGAGGATTCCCTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGCTGAGTGCACATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCCCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAGACGTGTG
CAAATTGGACTCTGTGCTGGGGACACGGTTGTGAACATTGTGTAAGCAGTGAAGGAGATTGTTGTG
GCCAGTCTTGAAGTTATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAGTATAG
ACCATGGCTGTGAACACATTGTGAACAGTGCAGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGAAACGCTGCCAGGAAGGAGATGTGCAAATCAACCCACCATGGCTGCGAACACATTGTGTTA
ATAATGGGAACTCTACATCTGCAAATGCTCAGAGGGATTGCTCTAGCTGAGGACGGAAGACGGTGCAGAAT
GCACTGAAGGCCAATTGACCTGGCTTTGTGATGATGATCCAAGAGTCTTGAGGAGAAGGAAATTGAGGTG
TGAAGCAGTTGTCAGGAAATTAGATCTTGTGACAATTCCCCAAAGCCGCTCAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCTCAACTCAGCCAAAGACATGAAAAAAAGCCGTCGCC
ACATGAAATACATGGGAAAGGGCTCTAGTACTGGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGCCAGGCCCTTCACAAAGGGTGCCAGAGCAGCCATTGTGTTCACCGACGGACGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCAATGGTATCACTATGTATGCTGTGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCTCTGAGCCCACAAACAGCATCTTCTATGCCAGACTTCAAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAACGGTCAACAGCCAAACAGAACTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGTGCAACACAGATATCTGTTGAAGAAGACAATTTCAGGTCTACACAAAAGCTTT
CCCATTCAACAAACCTCAGGAAGCCTTGGAAGAAAACAGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTGTTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGTATTGTTAAATCAATAATGTGAGTAAACAAATCAGTACTGA
GAAACCTGTTGCCACAGAACAAAGACAAGAAGTATAACTAATGTTAAATTATCTAGGAAAAAAACCT
TCAGAATTCTAAGATGAATTACCGAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTAGAATATACTGTGGACAC
AACTGCTCTGCCCTCATCTGCCCTAGTGTGCAATCTCATTGACTATACTGATAAAAGTTGACAGTCTTACTT
CTGAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGAAACAAGTGGATTTTATACAATATTAAAATCACCACCTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLIDGPDVTRVGLLQYGSTVKNEFSLKFKRKSEVERAV
KMRHLSTGTMTGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAI GVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDS CALGDHGCE
HSCVSSEDSFVCQCFCGYILREDGKTCRRKDVCQAI DHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRCKDVKSTHHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHM FERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDS DGRQDS
PAGELPKTVQQPTESEPVTINI QDLLSCSNFAVQHRYLFEEDNLLRSTQKLHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTCCGGCTGGCGCCCGTACTCCGTCCGGCTGGGGCTGA
CATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCCGTTTGTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGGCCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTTGACTGGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCG
CATGGGTGCTGCTGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTC
TTATTAAAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATACTAA
TGTGGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISPIPGGVSSGLSR
MGAVPVMPVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCCTCCGCTCCTAGTGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAAATTGCACCAAGACACCTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATATTAGCTGAATCATCTTCACTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCCCTTAACACTCAACTCTTACTGAATTGTAAAAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTTATATTATA
AGAGTATTGGTCCTTGCTTCACTGACAACCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACTTGAACAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCTTTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTCAGTATTGCTTGCCATATGCATTTT
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTGTTGGATCAATACAAATACTATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTG
ATTGAAGGCATACATCTCTATCTCATTGTTGGTGTCACTACAACAAGGGATTGGCA
CAAGAATTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATAACAGATATTGGCACACCAACAAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGAGCCCTCGCTTTCTGTCCTCTGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTCAGCATTGTTGTTACAGCTTACACTTCAGTCAGCAATGC
TTTCCAGGGATGTTCAATTCTGTTGTTATCTAGAAAGATTCAAGAACAG
ATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAAGGTAACATAGAGAACATG
GTGGATAATTACAACACTGCACAAAATTTCAAGCTGTTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACACTGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCCAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACATGAAGGGCAGA
ATATCAAACAGTGAAAAGGGATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAAGAACACATTACCACTTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACTTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGYYCMCVPGRSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVEVYRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRIQSFFQKTTEFDT
NSTDIALKVFVFFDSYNMKHIHPHMNMDGDIYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITYFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAFWMCIEGIHYLIVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGAGGAGTTCCCCGAAACCCGGCCG
CTAACGAGGCCTCCTCCCGCAGATCGAACGCCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAACGCCGCCCTGCCTGCCCGGGCCGGGGAGGGGGCTGGGCTGGGCCGGAGGC
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTGGCACCTACCCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCCGTCAGAGCAGGAGCGCTGCCAGGATCTAGGCCACGACCATCCAACCC
GGCACTCACAGCCCCGAGCGCATCCGGCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCCGAGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTCCACGTATGG
ATCCTGCCCGGCCCTGGCTGGCCGTGGCCGGCGCCCTCGCCTCTCGGACGCCGG
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTCCTGCCGATCCGTGCCGACGGCGTGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTTGCGGACCGTGGCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCACAGCGGAGCTGTACAAGAA
CAGAGGTTTCTCCACTCTCATTTCTGCCATGCTGCCATGGCTCCAGAGGAGCCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAACT
GAGACCATGCCGGCCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGAGCTTGCCTGAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTATGTCAGCTGAAGATTCTCAATTCTCATCATT
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGGAAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCA
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGACAACCTGAGAATT
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGCTCCGGTGTACCTGC
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGGCCCCACCTTATGTCACACTGCACTTCTGTTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCATAACTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAATTATATTATGATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGGAAGATGGCAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGGCTATTTAGCCTGAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTCGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTACACAAATGAATACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT
TGTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTACGCCTGTAATCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCACTGGCCAATATGGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAAATACTGGTTTTACCTGAGAATTCTTACAATAATAGCTGATATT

FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
LLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDL
NISGIIAAVVVVA
LVISVCGLGV
CYAQRKGYFSKETSFQKSNSSSKATTMSENVWLTPV
IPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACATCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTTCTCCAAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCCTATTGAACCTACTAGCACTGACTG
TGGAAATCCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGGAAGGACATGCCACT
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAAATTATCTCAGTCACCAAT
ATTAATGTAaaaAGATGCCCTAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCTGAAAATGTCTGCGAACACTGAGCAACTTACAAGAACTCTATATTAACTACA
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTTTTACGATAACAGGCTTAAAGTACCCCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTTCAGCAATATGCTACACTTAAAGAGTTGGGATAAATAATATGCC
GAGCTGATTCCATCGATAGTCTTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATAACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAAACACATTGATTCACTGGAGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGTAGAATGTTGGCAAGTGCATTCAAGGGACATGATGGAAATTG
CTCCCTTCTATAGCTCTGGAGAGCTTCTTAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAAAATGGCGTAACCTCCAAAGAAGGGGTTATATACTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTACCAACAAATATGTCCT
AAAAACCAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFPVNLTLGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRLSIVAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAKYHTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCAGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGGATGAAACATGCTGGCAGACCATTCCCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCCATCCATTGAAACACATTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSGGLNVTC SANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCATCCTCCTGCTGGTGCT
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCGAGGGCATCCCCACCGAG
ACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG
CCTTCAACAACCTTCAACCTCCGGACGCTGGTCTCGCAGCAACCGCTGAAGCTCATC
CCGCTAGGCGTCTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGCC
CATCGTCTGAGGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCGCCACCTAGTCTATCTCGCTCCTCAACCTCTCCTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTCCGGCCTCAACTACCTGCCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTCGG
CGCCGCTGGCGGCTCAACTCAACCGGAGCAGCCCACGTGCCACGCCAGTTGTC
GGGAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCC
CCCGCATCCGGGACCGAAGGCCAGCAGGTGTTGTGGACGGGCCACACGGTGCAGTT
GTGTGCCGGCCGATGGCGACCCGCCATCCTCTGGCTCTCACCCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGCCAACGCCGGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGAGCTACTGCCCGACTGGCCCCATGCCAACAA
GACCTCGCTTCATCTCAACCAGCCGGGAGGGAGAGGCCAACAGCACCGCGCCACTG
TGCCCTTCCCTCGACATCAAGACCCCTCATCATGCCACCACATGGGCTTCATCTCTTC
CTGGCGTCGTCCTCTGCTGGTGTGCTGTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGTCGCCACCTGCTCAGTCTCCAGTCTCCACCTC
CTCCCTACCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGTCCCTGCTGCC
CCAGCCCTCACCACCTGCCCTCTACAGGACCTCAGAAGCCCAGACACTGGGACCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTACGAACATTCTGTAACTTGGTTCAATAATTATGGATTT
TATGAAAACTTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVL
EISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEG
SMLHELRLQEIQLVGGQLAVVEPYAFRGLNYLRVLSNVSGNQLTTLESVFHSGNLET
LILDSNPLACDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFT
CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTV
FPDGTLLEVRYAQVQDNGTYLCIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTF
AFISNQPGEGEANSTRATVPFPFDIKTLIATTMGFISFLGVVLFC
LVLFLWSRGKGNTKHNIIEIYVPRKSDAGISSADAPRKFN
MKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACGCGTCCGCACCTCGGCCCCGGCTCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGAAAGCGCGATGGGGGCCAGCCGCCTCGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCACAGAGCTAGCATCAGC
ATCAGCAATGTGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCCGAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGAGCATCGTGTGCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGCGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTCCCT
CCTCCTCCAGCACCTACCAACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGAAAAGGCTCCGACGATGCTCCAGACGCCAGACGGCATCATCAATGCGAGAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATTAGAGGCGCCTGCCACTCCTGC
GCCCGAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGCTGC
TTGGGTGCGTTTGACTCGGTTGGAATGGGAGGGAGGGAGGGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCAATTGGTTATTATTATTTGAAACATCC
CAAATCAAATCTGTCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGGCAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCCGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCACTCCCAGTTTACCATTTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACTTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTGCAATGAAATCGTCCGGGGCTTCTGGGCTGCAAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCAGGCTGATTAAATTACGAGATATAGACCCGGGGCTTCAGG
ACTTGAACAAGCTGGAGGTGCTATTAAATGACAATCTCATCAGCACCCACTGCCAAC
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGTCTGCGAAGCCCCACCAAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTGGAAAAACCGAGTGAGTGGATTCTAGTCTCCGGGCCCTG
CCCAAGAACAGAACCTTGCTCCTGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTGCACCATCCCAGGGTCGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCCCTACGAGATAACAAGATCCACAGCATCCAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTTCAAG
AACCTTTGGACCTCAGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCCGG
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACTG
CTGAGGTCCTGCCGTGGACGTGTTGCTGGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCAGA
TAGACCTCCACGAAACCCCTGGGAGTGCTCCTGCAAAATTGTGCCTTCAAGCAGTGGCA
GAACGCTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAAACAGCACTGGGTTGGCGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCCGACTGCTGCTGGT
GTTTGTACCTCCGCCCTCACCGTGGTGGCATGCTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGGAGATGCCAACTCCTCCGGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTCCTACTGGCACAATGGGCTTACAACGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCCTGTGGGTTGGATGCCGCGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDCVKCKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTFFKTNGQEDHATPGSAPNGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMCNNRNVSSLADLKPK
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLLLVFVTSAAFTVVGMLVFILENRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCGCGCCAGCTGTGTTCTGACCCAGAATAACTCAGGGC
TGCACCAGGGCTGGCAGCGCTCCGACACATTCTGTCGCGGCTAAGGGAAACTGTTGGC
CGCTGGGCCGCGGGGGATTCTTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGAGGG
AAGGGAGGGGAACCGGGTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCGCTCTGGCAGGCCCTCTGGCCGGCG
CGGCGAACACCCACTGCCGACCGTGCTGGCTGCTCGGCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGAGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCTGTGCTCGCCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGCTCCAAAGACCTGCTGTTCTGGGTCGACTGGAGCGCAGGCCGTTCCACT
GCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCCTGGCTGTCCTCCGACCCGGCGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCAACGGCTACCTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGCCTAGACGACTTGGGAGG
CTTGCGCTGCAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTCTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACAGCGCCGCCGCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAACAGCTGGGAGAGAC
ACCACTGTCCTGAACAAGACAATTCACTGAGCTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCTGCACTCCTCAGGCTTT
CGACTCCCTCTGCCGTGGCTTCATATTGTGAGCAGCAGTAGTGTGTTGGTGT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCCGGCCTGGAGAGTGAACCTGAGGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCCGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCTCTGGCTCTAGTGTGATGCAT**AGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATGAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACGGGTAGTGCCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTGGAGAAGTGAACCTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACAAAATGGAAAGGAAATGTTCTATGTTCTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAKGCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATCGCCTTAAAGTGCCTCCGCCCTGCCGCCCGTATC
CCCCGGCTACCTGGCCGCCCGCGCGGTGCGCGCGTGAAGAGGGAGCGCGCGGGCAGCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCGAACGCCCTGGCGCCACTCTGCCCTGCTGCTGGCTGCCACCCAGCTCTGCCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGCCATGCAATGCCAGCGCATTGCCG
CTTCTGTGGCACCTTCCGCCCTGGAGCCCTGTGTCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACCGGGATTACCCCTGCAGGAGTCACCTGTGTGGCACATTGTAGCCC
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCCAATTGTGCTGAGAGAAATGAACTTCTTATTCACT
TTTATCAGACTTAAGTTAACTGCAGATGGGTTATTGGTCACTACATATTAGGCCAAA
AAACTGCCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCATGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCCTCAGAACAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAACGCTCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAACTGTGTCATTAAAGCTGTATTCTGCCATTGCTTGAAGATCTATGTT
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GAATGGTTGACTCTCACATGATGGAGGTATGAGGCTCCGAGATAGCTGAGGAAAGTTCTT
TGCCTGCTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTAGAAGTGAATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTCGTCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGCTGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCCCGGACCTTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAAACAGAGAGGCCCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGCTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGA
TATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPAGTERPCGGYGCQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCAGDQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGAGCCTGCTGCGCAGCTGAGCTCAAAGAGGT
GCCAACCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTC
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCGGCTCTCCAGG
AGCCGGTCCCCAAGGCCCGCTGCACAGGCACGGGCGGCTGCCCCGCGCAGCGCCCGGGC
CGGGTACCGTCAGTGGCTGCGCTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTCAGAGG
GAGCATCTGGCCCGCTGGCGTCCGGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGC
GCCAGCCGGCTGGGAGGCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGGAGGCTCCAGCCATGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGGAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGCTCTAGGAATGAGAAATCTTGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTACTGCACTATATTCTAAGCACTTACAT
GTGGAGACTGTAAACCTGAGGGAGAAAGCCCANTGTGTCATTGTTACTTGTCTGTCAC
TGGATCTGGCTAAAGTCCTCCACCACCTGGAACCTAAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT
AAAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQSVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTCTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACACAAGATGGTCCCCACCTCTGAATAACACCTGGTTCAAAGAT
GGGATAGTGTGATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTTCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCAGTTCACAGGATGCCTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCATTGTACTGAC
GACCAGGGCCAGCTGTTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCATCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCAGTAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTAAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGAGGCAGGGATCACCTGAGGTGGAGTCAGGCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELEVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCAACCCACCAAGTCCAGTGCCGACCCAGTGGCTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACGCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGGCCCTGTGACCCCTGGAGAGTGTCCCTCTCAGGAATGCC
ACAACCATGGGGCCCTGTGACCCCTGGAGAGTGTCCCTCTCAGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCAACTTGCACCCAGCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCCGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCGDHPDCPDSSDELCGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGGTCCGGTCTCGCTCGCGCAGCGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAGCTGGATGCCCTCTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGCTGACCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGCTCGGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGCCACTACCTCAAATGGTAGTCACGGAGATTCTGCT
GCCACCCGGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGCCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGCACCTGACTTGTGGTAGACGGCGTCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGGTACATGCCCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAAGAGGCCACTTCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGACCCACCCCTGCTCGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCCACGGT
GTTGTTCTTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTCTCTGGTTTAGACAAATGTAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASNDPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACACGCGTCCGCTCCGCCCTCCCCCGCTCCCGTGCAGTCGGTCCGGTGGCCTAGAGA
TGCTGCTGCCGCCGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTGTTA
TAAAGTCATTTACTTCATGATACTTCTGAAGACTGAACACTTGAGGAAGCCAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACTGGTATGGATGAGCCGTGCAGCAGGGTCTGGTGGTATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCTTGCAAATATTCTGATGAGAAACCAGCAGTTCCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAAGCTGCCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTTGTGGTACCCAGCTGTACTTCCAGAAGAACACACC
TGGCCCTCTCCTCACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCTTGAGTGTGGT
CGGGAGAAGCCACTCCGATGACATGTCTTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAATACACAGAAGGTCTATGAAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAAGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAGATGGCTGTGGAGCTGGAAAACACCTCTGTTCTGCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTCAAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGQLVSIESEDEQKLIKEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATCACTGGTGT
GTTCAAGCATGCGCTTGTGGACCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAATGGTCAGGTCGTGTTCGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCCCTGGAGGAGCAGGTAGAGTGGAAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGTCTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACGAGGCCGGAGGCAGACTGCCCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACAGCACCTGGAATCTAAGGAGTGTTGTCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAAGTGCCTTATAACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGAGCTAAACTAAATATTGCTGCTGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTGATCCTT
GCCATTGCAACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCCTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCCCAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCTG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCAGTG
GAGGTGCTGCACAAGGGCTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCCTCTCCCTCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCACAGATTTGGGGTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGCTGCCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGAAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAATTCTGAAATTGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQCQGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCGGCGACCGGTGGGCGGACGGCTGGGCGGCTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCCGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTTCTCAGCCTCATGGCCTCCAGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGTTGC
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGTCTACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTGGCCGCATGGCCCAACTTGGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAALKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSI
LVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVS
VPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLE
PEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGGACCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCAGCTCGCCGCACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTCGCTCCCTACAGAAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCATTATTCACCCCTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCAGCTCAGATAAGCCAGAAGATGCCAGTAGTTCTGGCTACAGGGTGGCCGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCTTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCAACGCTCTCCATGTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGAAATATGTGCCAGCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAATAACTGGATAAACTACTAGATGGCAGTTAAC
AAAGTGATCCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTTCGACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAAGTACTTGGAGA
AGATAACAGTACAGTCAGTTAAGCCATGGTTAAGTGAATAATTATAAGGTTCTGA
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGTGACTTCCATCAGGTAATTATC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGTACATGATTAATCGA
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGAAAAACAGAAAATGTCAAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTGAAACAAGTGAGC
TTTGTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA
AATTTTAGGTCTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGGTGCAGTTG
TAACAAAACAAAGCTGAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
S
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
G
GPYVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
F
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLNPREVKINLNGIAIGDGYSDPESIIGG
Y
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWEAFEILDKLLDGDLTSDPSYFQNV
C
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNNQTFNDGTIVEKYLREDTVQSVKP
E
WLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIR
Q
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCGGAATGGCACATGTGGATCCCAGTCTTGGCTACACAT
TTTCCCTTCCTAACAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGTTCTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGACTCTCACTCAGGGTACCGAGCTCCTG
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAGCTTCAAAACAGGAGCAGTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAGACTGGGTTAGCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACAAAATAGATAACAGGATCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
AAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCCAGGATGGGACCTGGGTC
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGGTCTGCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTCCACTCTGAGAATCGTGAUTGGACCTCAACCACTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCAGAAGAGGACAACAAGTCTCGTACCCG
CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCACAAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTTACCAAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTCAGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGCTACTTTCTCACTGTCCAGCCGAGA
CCCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTCTCACACCTCACGCATGTGCGG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCTCCCTGCCCTCGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTCAATATCACCAGCCAGGACGATGACTCTTGCATCTTCCATCCAAAGGGCAGAAG
CAGTATCACCACCGCCCGATGACTCTGCCCTGTGCGCTTCCATCCGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCTGCTACCAAGGGCAGGGCACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTACAACGGCTACAGCGTGGTTTTG
TGGGGACTAAGAGTGGCAAGCTAAAAAGTAAGAGTCTATGAGTTAGATGCTCAACTGCC
ATTCACTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAAGAAGGGTTAATTGTG
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAFCPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCAGCTGGAGTGGGAACCCGGTCCCCCGCCTAGAGAACACGCG**TGACCA**
CGTGGAGCTCCGGCGAGGCCGGCCCGCACGCTGGACTCCCTGCTGCTGGCTTGGCTTCCTGGTGCCTCC
GCAGGCTGACTGGAGCACCTGGTCCCTCTGGCTCCGCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCTGTGGCTGAACACCCCTCACCACTATGTTCCGTGGAAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAACCTGGACCTGGAGGCCCTCGTCTGATGGCCAGAGATCG
GGCTGTGGGTGATTCTCGTCCAGGCCCTACATCTGCAGTGGAGATGGACCTCGGGGCTTGCCCCAGCTGGTAC
TCCAAGACCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAACAGTGGACCTTATTGACCACC
TGATGTCCAGGGTGGTGCCTCCAGTACAAGCGTGGGGACCTATATTGCGTGCAGGTGGAGAATGAATATG
GTTCCCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCAGTGGAGGACCGTGGCATTGGAACACTGC
TCCTGACTTCAGACAAACAAGGATGGGCTGAGCAAGGGATTGTCAGGGAGTCTTGGCCACCATCAACTGCAGT
CAACACAGCAGCTGCAGCTACTGACCACCTTCTTCACGTCCAGGGACTCAGGCCAAGATGGTGTGGAGT
ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACCTTGGCTTCATGAATG
GAGCCATGCACCTCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACGGCG
ATTACACGCCAAGTACATGAAGCTTCAGGACTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCCACCTG
ACCTTCTTCCAAGATGCCGTATGAGGCCCTAACGCCAGTCTTGTACCTGTCCTGTGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCACTCAATGGGAAATGGACAGTCCT
TCGGGTACATTCTCATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGAGG
TGTGTTGTGAAACACAGTATCCATAGGATTCTGGACTACAAGAACAGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCATGAAATGATTCAACCCCTGAAAACAGAACACCCACATTACCTGCTTCTTGG
GTAGCTTGCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTACATGTTTGAGGAGACGATGGGGCCCTGCATTACAGTTACGGAAACCCCC
ACCTGGCAGGAACCAGTACATTAAGT**GAGCGGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCCTC**
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCACCCCTCACTGCAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTAAAACCTAACGCTGCAGGGAAAGGTGGGATGGCTCTGGCC
TGGCTTTGTGATGATGGCTTCTACAGCCCTGCTTGTGCCAGGGCTGTGCTGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTGCACCGGAGCTCACAGCCC
TGCGAGCATCTGCTGGACTCAGCGTGTCTTGTGGTCTGGGAGGCTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCTGGTGTGTCACCACTGAGGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCAACACCTCTGAGCCTTCTTGGATTCTGAAGGAACCTGGCGTGAGAACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCACAGGGTGCAGGGCTGGAGAACAGAACATGTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTGGTGTGAGTGGAGGACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGACATCC
AGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGACATCCAGGG
GGAGGACAGAACGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGACATCCAGGGAGGAGG
ACAGAACGCCAGCTAGTGGCCCCGCTCCCCACCCCCCACGCCGAACAGCAGGGCAGAGCAGGCCCTCCTTC
GAAGTGTGTCAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGCTCACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRRPARTLGLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPMRRLTTYKGFTEAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDKGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEMYWTGWFDSWGGPHNILDSSVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFYIYE
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQQYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPPLKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGAGGGGGTGGACGGGTCAGGAC
CTGGTGAGGGTTCTCTACTTGGCCTCGGCTGGGGGTCAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCAGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGCCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCCGCCTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTCGTTGTAAGGGGTCATGACCGGTTCTCTAGACGGGGCC
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTGTCTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCCAACGCCATACAGTTATGTGCCCTGGAAC
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTGAG
TGGGAGATGGGGGTCTCCCATCTGGTTGCTTCGAAAACCTGAATTCAAGAAC
AGATCCAGACTCCTGCCGAGTGGACTCCTGGTCAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGACTGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCCGT
CGGAAGTATGAACCCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAGGACTAGAGAACATGC
TCAAGTTGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTCCGATAAGAAGGGACGCCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGTCTTGGCCCCGTGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC
CATGACCGTGCTATGTGATGGTGGATGGGGTGTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAATTCAAGGGCTGTGAAGCCACCAATTCTG
GGGCAACAAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTTTCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAGTGGGACTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCCGTCCTCAACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAACCTCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGGCAGAGGTTGCACTGAGTGGAGGTTGTAACACTGCACACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPSPKMM
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFLYRTYMTHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVWKWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTC
ACCCACAATATGGCTTACATGTTGAAAAAGCTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAAACGATTT
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAGAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCTGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGTGTATTTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACCTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCTAAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAACCCACATGCTATTTCAGCCTCTCTAAATTACAGGAACGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCCTCTAAACAACAAGCTCGAACCTTACAGTGGCAGTATTT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGTTGTTG
TGGAAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGGTTTAAGTCATTCACTTCAAATCATTGTTCTTTAAATTGTTGTAACGGAT
AAAGGGAAGGAAAAATTATAACTAAATCTTGGTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLLESRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCCCGGTCGGGCTTCTCTGGACTTGCATTCCATTCTTCACTGACAAACTGACTTTTTATTTCT
TTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCCTGGAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTCTCCTCCCTGACATTGGCATTGCTTAGTGGTGTGGGAGGGAGACACACGTGG
GCTCAGTGCCTGCACTTATCTGCCTAGGTACATCGAAGTCTTTGACCTCATACTGATTATGCCTGTC
ATCGCTGGTGGTACCTGGCCCTGCTCTGCTGATAGTTGTCGTGCTCTGCTTTACTCAAAATACACAAC
GCGCTAAAAGCTGCAAGGAACCTGAAGCTGTTGGCTGAAAAAACTACAACCCAGACAAGGTGTTGGGCAAG
AACAGCCAGGCCAAAACCATGCCACGGAGCTTGTCTGCTGAGTGAAGGGATATAGAATCTGTGCC
AGTTTGATTCCCTGCCACCTTGTGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCTCTCAAA
GCAGAGGCCCTGAAGACTCTAATGATGCAATGAGGCCACCTGTTGTGATGTCAGGCCACAGAAGAAGGCCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGAAACAGCTGCTGGAGATCCTACAGAGAGCTC
CACTGGGGCAACCTTCCAGGAAGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACCACTGCA
CACAGCTGCTCTATTCTCACAAATCTACCCCTGCGTGGCTGGAACTGACGTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTTAATTCTCTCTGTTGGGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTCCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTAAGTGAACACATTAAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGCTGCAGTAAAAGACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCCTTGCTCTACTACTTCTCTCTAACATCTCTATTCCAAACTGT
GGCGGTATACCTGGATACCTTGGAGGATCCTCACCAGCCCCAATTACCCAAAGCCGATCTGAGCTGGTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTTCAAAGAGATTCTTCTAGAAATAGAC
AAACAGTGCACATTGTATTCTTGCCTCATATGATGGCCCCCTCCACCAACTCTGCTGATGGACAATGCTGT
GGCGGTGTGACTCCACCTTGCATCAGTCAAAACTCTGACTGTCGTGTTCTACAGATTATGCCAATTCT
TACCGGGGATTTCTGCTTCTACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAACTGGGAAATACTTGCAACTAAA
GACCCAACCTGCAGACCAAAATTCAATGTTGGAAATTCTGCTCTCTTAATGGATGTTGACAATCAGA
AAGGTTAGAAGATCAGTCACATTACTACACCAATATAATCACCTTCTGCATCCTCAACTCTGAAGTGTAC
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACACCAGCATGGCTCTTTGAATCCAATTCA
TTTGAAAAGACTATACTGAAATCACCATTATGTGGATTGAACCAAACCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGTCTTCTGATACCTGTAGAGGCCCTCCTCAACTCTGAAGTGTAC
TACGACCTAATCAAGAGTGGATGTAAGTGTGAGATGAAACTTGTGAAAGGTGATCCCTTATTGGAACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTTGGAGAAGTGTGAGCTCTGCTGATCTGCACTGTAAGGTTGATATGTGAT
AGCAGTGCACCCAGTCTCGCTGCAATCAAGGTTGTGCTCCAGAAGCAGAACAGAGACATTCTCTCATAAATGG
AAAACAGATTCCATCATAGGACCCATTGCTCTGAAAGGGATGCAAGTGTGCAAGTGGCAATTCTAGGATTCTAGCAT
GAAACACATGCGGAAGAAACTCCAAACAGCCTTCAACAGTGTGCACTGTGTTCTCTCATGGTTCTAGCTG
AATGTGGTGAATGTCAGCGACAATCACAGTGGAGGATTGTAATCAACGGGCAAGACTACAAATACCAAGAAGCTG
CAGAACTATTAACTAACAGGTCACCCATAAGTGGAGACATGTTCTCCAGGATGCCAAAGGAATGCTACCTG
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGCACACACAGGCCCTGCATGAAAAAAA

FIGURE 70

MELVRRILMPLTLLILSCLAELETMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCRVTPTFESSNSLTVVLS
TDYANSYRGFSASYSIYAENINTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGNST
VEIYYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCCG
GGACATGCGGCCCGAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGC
TGCTGCCGCCGCCGCGGTGCCCTGCCCACAGCGCACCGCCTCGACCCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCCGGCATCTCATCCACTG
GGGAGTGTGTTCCGTGCCAGCTCGGTAGCGAGTGGTTCTGGTGGTATTGGAAAAGGAAA
AGATAACCAGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAAATATGAAGAT
TTTGGACCACATTACAGAAAATTGTTAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGGCTTACCTGTGGGGGT
CAGAATATTGTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCTAGGAACAGAACTGACCTGCCTTGGACTGTACTATTCCCTTTGA
ATGGTTTACCCGCTTCTGAGGATGAATCCAGTTCAATTCCATAAGCGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTTGGGGCACAGTAGTCACCAATGATCGTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTACCTGCAGTGCATCGTTAAACCCAGGACATCTTGCA
CATAAATGGGAAAAGTGCATGACAATAGACAAACTGCTCTGGGCTATAGGAGGGAAAGCTGG
AACTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG
GAGCAGTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCATGCCATTCTTCTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC
GATTTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACACTGGATAAGAAAATTATTGGCAGTTGAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTTGAGGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCGGGTGAGTCAGTGAAGTGAAGGCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTCAATTATAAACATAAGTGTACTGTAACCTACAAACGTTAATT
TTAAACCTTTGGCTCTTGTAAATAACACTAGCTAAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAATGGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGCCAAGGCCTTTGCGTGAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCAGACCAGC
AGCTGAATTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGTGGAGA
TGGATTCTGGTGTATCTAGGATTAGCCAAACCCAAGTGTGGAAAAATGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAATCGTCATTCCAGAAATTATCACCAACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTATTGTCAAGTGCAGTACACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAC
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGTCTTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTTACAAACAAGAATCAGCAGAAGGAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAGAAACTACCGTGCATGCCTGGAA
GCTGAAGTT**TAG**ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAAGGCCAAGAACCAAGAACAAAGTCCACCCCTT
GGTTCTTAATGGAATCAGCTCAGGACTGCCATTGAGCTATGGAGTGCACCAAGAGAACATGC
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCACTGGAGAAAGGAGTTTGCAAAGTCAA
GGACCTAAAACATCTCATCAGTATCCAGTGTAAAAAGGCCCTCCTGGCTGTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA
AGAGCAGAAAGAACATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGCTAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTAACAAAAATAAAAACCTTATAAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCTCA
GTTTGATATTCTAGCTTACTCTCCAAACTAATTCTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTATTAAACATACCTAAGAAC
TACATTGTTACCTCTATATACCAAAAGCACATTAAAGTGCCATTAACAAATGTACT
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNNPKCGKNGVGVLIWKVPVSRQF
AAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFKNNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATCGGTGCCGCGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTTCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTGC
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACCGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGGCTCAACCCCCACCAAGTGT
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTCGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTTGATTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGCTTCAACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTTGGCTAGTGTGTTACTGCTTATC
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCCAAGGACTCTTGCTTCTTAAGCCCTCTGGCTTGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTTGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGCTAGGACTTGGAGGAGAAACCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFMSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFKGVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCCGAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCCCAGAGAAGGACGTGCTGGTGGCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCCGTGCACCTGCCGAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCCGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTGGCTTCTTACCAAGTCCCCCA
ACGGGCGTACCAACTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGT
GTGGCCTCTTGAGCAGCTCTCCGGGCTGGGAGGGAGGGCTGGACTGGTCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTGAGAAGCT
GACGCTGACAGAGGAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCCCTGGAAGTTCCATGCCCTGGGACCGCTGCACGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTCACCCGATCCTAACTGTGGGCCAGAGCTGGG
CCGAAGCTTGCTTCCCCGACCCCGAGGCCGCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCCCTCCCTGCCGATTCCCTCACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCAATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTTGCCGGTTGTGGCTCTG
GAGGGTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGGCCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCCGCC
CACCTCTACTTCTGTGAAGGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGGAAATCTGAGGGAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAAATGGTGCTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGN GHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENG APEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVR SYGPR
HRR LHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHDGSEVGHVLPAPQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTCCGACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCTGTTCTTGTCGCTCCAG
CCTGTCGTCGTCGTTGGCGCCCCGCTCCCCGCGTGCAGGGTTGCACACCGATCCTG
GGCTCGCTCGATTGGCGCCGAGGCGCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGTCCTCTCCTCTGCGCCGCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGGTGCAGCGCGGGCCTCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCGGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACCAAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTGTGTATGGAACATAGTATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTCACAGTAACAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCGAGAAAGAAAATGG
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGAAAGCTTAATATTGGCAGC
GCCGATTAAATTACAGAAGAATTGGTGGAAAAGTGGCTTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCTTCAAGCCAGTGAACATCCAAAATAGAATTAACTTGAA
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACACATGCCAACTGGTTGGCACCAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACCATGAACAAATGATGTCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTGGTCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAAATGCTCTAGCTGTACAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGG
GATGCCATTCCCTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCCCTGCACTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAACCGAAGGAGTCTCACGCTTCTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTACAGAGGCAATTGTTAGAGATTCTAGAACCCAGCAAT
AATGGTAACATTGACAACAGAAAGAAAAGTACAAGGGATCCAGTGTAAATTGATT
CTCATAACTGAAATGCTTAGCATACTAGAATCAGATACAAACTATTAGTATGTCAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAGAACATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLMELFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGACCCGGCCCGCCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCG
GGCGGGCGGCTGCAGGGCGAGAGCGGAGATGCAGCGGCTTGGGCCACCCCTGCTGTGCC
TGCTGGCGCGGGCGGTCCCCACGGCCCCCGGCCGACGGGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGCAGGAGGACCCCTCAATGAGATGTTCCCGA
GGTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATGTGCACCGAGAAAT
TCACAAGATAACCAACAAACAGACTGGACAAATGGTCTTTAGAGACAGTTACACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTGCCAGCTTCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGGAGACAGCTGTGTCTGGGGCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCAGAGAGGCCTGCTGTTCCCTGTTGACACCCCTGCCGTGGAGGGCA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGAGCTAGGCCTGATG
GAGCCTGGACCGATGCCCTGTTGCCAGTGGCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCCTGTTGCCAGTGGAGGAGGTGCGCCAGGAGCTGG
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGCCAGGCTGCC
GCACTGCTGGAGGGGAAGAGATTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTTGCTTACAGGCTGGGCTGACCAGGCTTCTTCCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGCAATTGTTGAGC
TCCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTCTGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCAGATTATTGGCTGCTTGCCTCTACCAAGTTGGCAG
ACAGCCGTTGTTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGGAAATGTGGAGAAGAGTGCCTGCTTGCACAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTGATCC
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCCAAGTCACACAGCTAGTGAAGACAGCAGCAGTTCT
CTGGTTGTGACTCTAAGCTCAGTGTCTCCACTACCCACACCAGCCTGGTGCCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTGTTCTTGAGGCATGCACATCTGAAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAATTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAAATTGTTAGGGCGAGGATTATAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGATCCAGAGTTCTAAAGTTAAAGTTGCACTGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCAATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLLAWVAGATATPVVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARCDFHALPQLLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMNFRPLANLRSVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQMETLMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGRRPLPPAWFWGWSAPSVRVV
SAPLVLPWNPGRKLPRLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAACGGTGAAGAACGGTACCTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTCAAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTCATGGCTCATCTGCACTGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAACGACTCGCTTGAAGTCACTGCTGACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGGCGTCTCTGTGGAGGTGAGTGAGAACAGCTGGCAGCTGAACCTCAACAAACGAGTGGAGCCT
GGACAAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCACGCTGACCATCCCGCC
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTTACACACAGCGGCAAGATTGAAGCGCCTGCGCT
GGCCTTCCTGCGCAGAACCTGGGGCCTGCACATCAAGTTACCGACATCAAGGAGATCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCACCTGAGCGCGAGAACAAACCGTACATCGTCATCGA
CGGGCTCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAACGCAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGCAAGAACGCTGTCATCAACAATGAGGGCACCAAGCTCATCGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACTTCAGGGAGATTGACCTCAAGGACAACACCTCAAGGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGGCTTAAGCTGTGGTACAACCCATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGAACAAAGATCGAGAACGATCCCCACCGCTTCTACTGCCGCAAGCTGCG
CTACACTGGACCTCAGCCACAACACCTGACCTTCCCTGCCGACATCGCCTCCTGAGAACCTCCAGAACCT
AGCCATCACGGCAACCGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGCGGAAGCTGCGAGATCGAGCTGGGG
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGGAGGGCAGGCCAGCTAGCTCTCCAG
AACTCCCGACAGCAGGACAGCCTCGCGCTGGCAGGAGCCTGGGCCCTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCCTCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGCTCCTCCCTGGAGGGCAGCTGCCCCAGGGCTGAG
CTGCCACAGAGGTCTGGGACCCCTACTTTAGTTCTGGTATTATTCTCCATCTCCACCTCTCATCC
AGATAACTTACATCCAAAGAAAGTTCAGCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCTTTTCCCC
TTGTCTTATTAGCGATGCCCGGGCATTTAACACCCACTTGGACTTCAGCAGACTGGTCCCGGGCAACCC
CCATGGGACGGTCACCCAGCAGTGGCTGGCTCTGGTCCACGGGAGAGCAGGCCAGCTGG
AAGGGCAGGCTGGAGCTGCCCTTCAGTTTGTGGCAGTTAGTTTTGGTTTTTTTAATCAA
AAACAATTTTTAAAAAGTTGAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGCCAGTGAAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGCGCAGGGTGTCTCCGGATCTGGTGTGACCTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTGTGTTGGTTTTGGTTTTGGTGTCTGTTCTTCTCCTCC
ATGTGTCGGCAGGCACTCATTCGTGGCTGTCGGCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGGCTAATCCCGATGAACGGTGCCTCATTGCAACCTCCCTCTGCGCTGCCCTGCCCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCACCTCGGGCATGGTGT
CCAGTGCCACCGCTGCCCTCCGCTGCTCCATCAGCCCTGTCGCCACCTGGCTTCAAGAGCAGACACTTA
GAGGCTGGTCGGGAATGGGAGGTGCCCCCTGGGAGGGCAGGGTGTGTTCAAGGCCGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCCAGTGGCACCTGGTGGCTGGAGGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGCTGTCCGTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAAATCGTTACATGTGGGCTGAACTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLKLRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNkiekiPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGGGCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGTATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACTGGGTCAGTTATGTGAATGGTAGTGGTGCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTAGCGAGGGACCATAAGTGCACACTTGCGGGGT
TGCCTTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCTCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGCTAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGGCCTG
GGTGCAGAAACTGAAGTGGCCAGAACTGCCTAAATTCACTGAGCTGAAGTGGAGGCCCTGT
ACAGTGCACCTAAATCTTGGAAACATCTGCTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGCATATGGTCTTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTIONAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLANVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGAGGAGGCGGCCGTATCAGGACCATGCCCGA
CGGGTCATCAGTCGCGATCGTGGGTGGAGAGGACGCCGACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTCACGGCGGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGTGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCCTTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGGTACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCACCCCTCCAGGAAGTTCAGGTCGCCCATCAAACA
ACTCTATGTCAACCCACCTTTCCCAAGTACAGTTCCGAAGGAATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAAGGGCGGGAAGGTGCCTGCTTCGGTGACTCAGGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGATTCAGATGGAGTCGGTGAGCTGGGGAGTGGGTGT
GTCGGCCCAATCGGGCCGGGTCTACACCAATATCAGGCCACCACTTTGAGTGGATCCAGAAAG
CTGATGGCCCAGAGTGGCAATGTCCCAGGCCACCCCTCCCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCCTGGCCGGGTCT**TGA**GCCTACCTGAGCCCATGCAGCCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTGTCTTTGGTAAAAACACATCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCVGVSLLSHRWAHLTAACFETYSQDLSQPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDALP
SPHTLQEVTQVAIINNSMCNHLFLKYSFRKDIQGDMVCAGNAQGGKDACFGDGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACCGGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTGCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCCACCAGGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAAATGTGGCTGATCTGGTGGAGGCCATCCC
CACTGACCCCTCCACACGGTCAAAAATGGCTTCTGGCAGCCGGAGCCAGAAGTGCCTATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCATTGGCCCCATGTGGACTTTGTGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCCGAAGCGATAACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTCGTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGTGCACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGGCCCTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCCCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTTGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCATG
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCTATTCCATGGGTGTCCGGAACCTCGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGGATCCTGTAACAGGC
TGGGAACACCAACTCCAGTTGCTTGAAGACTCTACTCAACCCCTGACCCCTTCCTATC
AGGAGAGATGGCTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGAA
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCAATAAGATGCTGAACTAGCATTTTGAAATGCCTCTCCCTCCGC
ATCTCATCTTCTTTCAATCAGGCTTTCCAAGGGTTGTATACAGACTCTGTGCACCA
TTTCACTGATATTCACTCCCAATTCACTGCAAGGAGACCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTTG
ACTACTCTTGCTTCTCTCATCAATTCTGCTCTTCACTGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCCTGGAAACAAATCACTGACA
TCTACAAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCC GGCGCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGGCGGGAACAGTGCTGG**CATGG**CAGGGATTCCAGGGCTCCTTCCTCTC
TTCTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTG
GCCTGCATACCGCCTCCCTGTCGCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTTATGTGGACCCCAGTGTCTAAGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACCTAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGCCAGGGTCTGGGTCTAT
TGAGGATGTGGAAGAGACAGCAGCAGAACGTTCAACGTGGCTGTCAAATCACTTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCTGGCAGCAATTAGGGTCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTTATTTCATCTGAACTTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
TAACIHDGKTYVK
G
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKG
WIKG
NANDIGMDYD
Y
A
L
L
E
L
K
K
P
H
K
R
K
F
M
K
I
G
V
S
P
P
A
K
Q
L
P
G
G
R
I
H
F
S
G
Y
D
N
D
R
P
G
N
L
V
Y
R
F
C
D
V
K
D
E
T
Y
D
L
L
Y
Q
Q
C
D
A
Q
P
G
A
S
G
S
G
V
Y
V
R
M
W
K
R
Q
Q
Q
K
W
E
R
K
I
I
G
I
F
S
G
H
Q
W
V
D
M
N
G
S
P
Q
D
F
N
A
V
R
I
T
P
L
K
Y
A
Q
I
C
Y
W
I
K
G
N
Y
L
D
C
R
E
G

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCCTGCTCCCCGCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCTGGTGGAGC
CCCACCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCTGCCATCTGCCTACCTGATGCCTCATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAAGATCGTGCAGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCCTCTAGGGCGAGCGGGACGCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCCTCGGGCGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAGGAAACCCCTCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTGTAACCCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT
CTCCAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI CLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCCAC
AACAAAGGAGCGCGGGCGCCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAACTGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTCCCAAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCCTGCCAGGTGCAAGGGCCCTGACA
AGCCTAGCGTTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCAGCTGTCCCTCTGTCACTTCCCCACCCCTGCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACC
ATCCTGGAGGCACAAGGCCCTGGCTGGCTCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT
CACTGCCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTCCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEELAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCPSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHLPSLDEEPVTFPKSTHVPPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVGGLNSGPGHVWGPPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTAGCTAGGCTTTCAATTGGAGGCCCCCTAACAGAACCGTCATTCTCCAAGTTATGGTGGACGT
ACTCTCTGTGTTCTCCCTGCTTGCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAAGCCCTCGAGAAGTGAAGACTGAACAACAATGAATTGGAGACCAATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCCTTGCTGGAAACAGGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTGCTTGCACATTTCAGGACCTTAGCAGCAACAAATATTCAAGGCTCAAACGATTGCA
TCCAGCCCTACAGCTAAATATCTGATCTCAACAGAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGGCCAACACACTCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAATGAGATGGACTGACATTCCAAGGCCCTGG
TGCTCTGAAGTCTGAAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAATTTCAGCTGGACATAACAACCTAACAGAGATTACCAAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAACGTCAG
TGAGCTGGACCTAACTTCAATCAAGGTTAGATGATTCAAGCTCCTGGCTAACGTTACTAAATAC
ACTGCACATTGGGAAACAACAGAGTCAGCTACATTGCTGATTGTCCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTGCTTCTCTGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATGGATCGGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCCTTTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGGAAACAAACTT
TCAGAGCTTGTAAATGCCAGTTGTCCTCAGCTGCTAAAGGAAGAACATTTGCTGTTAGCCAGA
TGGCTTGTGTGATGATTTCACAAACCCCAGTCAGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCTGATTTCCCAATGACTTTGCTTGGAAAAAAAGACATGA
ACTACTGCATGATGCTGAAATGAAAATTATGCACACCTCCGGGCCAAGGTGGCAGGGTGTGATGGAGTATACCAC
CATCCTCGGCTGCGCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTGGTC
ATCCTACTCTGTCAAAGCCAAGCTACAGTAAATATGCTCCCTCATTACCAAGACCCCCATGGATCTCACCAC
CCGAGCTGGGCCATGCCACGCTGGAGTGTGCTGTTGGCACCAGCCCCAGATAGCTGGCAGAACGGA
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCACTGATGCCGAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGC
AACTCTGACTGTCCTAGAAACACCATCATTTCAGCTGCCACTGTTGGACCGAATGTAACCAAGGGAGAACAGC
CGTCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACACTGGACCAAAGATGATAGCCCATTGGTGGT
AACCAGAGGCACTTTTGCACTGAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGCTGGAA
ATACACATGTGAGATGTCACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCTCAGATGACGCCACCTCGTTAGACGATGCCAGGGACTGTTGGGTGTCATAGC
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGGTGTCATCATATACCAACACAAGGGGAGGAATGAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATAATTCTAGTTATTGTCATCTCAGGGAAAGTT
AGCTGACAGGCAGGATGGGTACGTGTCCTCAGAAAGTGGAGGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTCCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC
CACAGATGTTCTTGTCCGTTGGATCCACAGGCCCTATGTATTGAAGGGAAATGTGATGGCTCAGA
TCTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTAATGGACCACTATGAGCCAGTTA
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTCAAGAACATCTGCAACGGAGCTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCCTTTAGATTTAGTGCAAAATCCAGAGCCAGCGTGGCTCGAGTAATTCTTCTATGGG
TACCTTGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTATTCTCCCCAGACTTGACCTTAAACAGACTTTAGAAAACACTACAGGACTCCAAATTTCAGTC
TTATGACTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAAATCTTATGTTTAAATGGAGTTATGAATTAAAAGATAAAATGCTTATTATACAGAT
GAACCAAAATTACAAAAGTTATGAAAATTTCAGGAAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTAACTTTGTTATGCAAAAAGTATCTTACGTAATTATGATATAAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGTCACCAATT
TTAAATAGAAGTTACTTCATTATATTGCACTTATATTAAATAATGTCATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSSLRLLDSSFLGLSLLNLTIHGNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLCDCQLKWLPPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGTVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTIILRLREVEFASEGKYQCVISNHFGSSYSVKAALKTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLRTVKGTAVALQCIAGGSPPPKNWTKDDSPLVVTER
HFFAAGNQLLIIVDSDVSDAGKYTCMSNTLGETGNVRLSIVPTPTCDSPQM TAPS LDDDG
WATVGVIIIAVVCVVGTSLVWVIIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCPDPRTVLMHDYEPSYIKKKECYPCHPSEESCRSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTCCTCGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGTTGGTGTCTGACATAATAATCTAAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAAGGATGTTGAAATGAAGAACCGAGGATTCAACAAAGAAAAAGTATGTTCTTCTC
TATAAAGGAGAAAGTGGAGCAAGGAGATACTTGGAAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTTCCTTCTTGAATTCCCACAAGAGGAGAGGAATTAAATAATACATCTGCAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAAGTTGGATTTCTTCATCAACCTCCTTTTTAAAT
TTTTATTCCCTTTGGTATCAAGATCATGCGTTCTTGTCTTAACCACCTGGATTCATCTGGATGTTGCT
GTGATCAGCTGAAATACAACGTGTTGAATTCCAGAACAGGACATAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTCT
GCTGGCTCTCAACTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACCTGCCCTCTGTGTGCTCTGCAGCAA
CCAGTTCAAGCAAGGTGATTGTTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAACTTGAGGCACTTGGAAATCCT
ACAGTTGAGTAGGAACCATCTAGAACCTTGAATGGGCTTCAATGGTCTGGCAACACTCAACACTCTGGA
ACTCTTGACAATCGCTTACTACCATCCCAGAATGGAGCTTGTATACTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAAACCCATTGAAAGCATCCCTTCTTATGCTTTAACAGAATTCTTCTTGCAGGCACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCTTGAAGGTCTGTCCAACCTGAGGTATTGAACTTGC
CATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTCTGGGAATCA
TTTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTCAAAAATGTGGATGATAACAGTCCCAGAT
TCAAGTGAACGGAATGCCCTTGACAACCTTCAGTCAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAAACACAGCTTGTGCCCCGGT
TAACACTCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAATGGAACAGTCAGTCAGACACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGAATGGTACGTTAAATTCAACAAATGTAACGTGCAAGATACAGGATGTACACATGTATGGTGAAGTAA
TTCCGTTGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACACTCCTTCTCTTACTT
AACCCTGACAGTAGAGACTATGGAACCGTCTCAGGATGGGACCGACAGAATACATGTTGAGGTTCCAC
AGTGGTCGACTGGGAGACCACCAATGTGACCACTCTCTCACACACAGAGCACAAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGAATGATATAAACAGTGGGATCCAGGAATTGATGAGGTATGAAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA
TCGGAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCGTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTGAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAACAAACATCAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTATTAAACATCTATTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLNLHENQIQIIVKNSFKHLRHLIELQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCIDIL
WLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAACTTTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTTGGCAGTTCTTTGGTTCCCTCCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCACCGC
GAGGGCCGGCGTGCACCCCTCGGCTGGAAGTTGTGCCCCGGCCCCGAGCGCGCCGGCTGGAGCTTGGGTAGA
GACCTAGGCCGCTGGACCGCG**ATG**AGCGCGCCAGCCTCCGTGCGCGCCGCGGGTTGGGTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGTGCAGGGAACTCGGGCAGCCCTCTGGGTAGCCGC
GAGCGCCCAGTCCCCACTACCTGCCGCTGCCCTGGGACTGAGCTGAGCTAAGCGCTAGCGCTT
CCCGAGCCACTCCGCTCTGGTCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
ATGAGCCACCTCAAGCCTCGAGAAGTGAACACTGAACAACAATGAATTGGAGACCAATTCAAATCTGGACCA
GTCTGGCAAATATTACACTCTCCTTGGCTGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACGAGTCACATCAATGGAACCTGGTATTTGACAATTGGCAACACA
CTCCTTGTGTTAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTAAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCCAAGGCCCTGGTGTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAAATTGG
CAGCTGGACCATAACACCTAACAGAGATTACCAAGGCTGGTTACGGCTTACGCTGAGCTGAGGAACTTCAT
CTCAGGCCAAATGCCATCAACAGGATCAGCCCTGAGCTGGGAGTCTGCCAGAAGCTCAGTGGAGCTGGACCTA
ACTTCAATCACTATCAAGGTTAGATGATTCAAGCTTCCCTGGCTTAAGCTTACTAAATACACTGCACATTGG
AAACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGCTTCCAGGTTAAAGACTTGGATCTGAAAGAAC
AATGAAATTCCCTGGACTATTGAAGACATGAATGGTGTCTTCTGGGCTTACGAAACTGAGGGACTGATACTC
CAAGGAAATCGGATCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCATAGACCTGAGT
GACAACGCAATCATGCTTTACAAGGCAATGCATTTCACAATGAAGAAACTGCAACAATTGCAATTAAATACA
TCAAGCCTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGAAAACAACATTCAAGGCTTGT
AATGCCAGTTGTGCCATCTCAGCTGCTAAAAGGAAGAAGCATTGGTGTAGCCAGATGGCTTGT
GATGATTTCCTAAACCCCAGATCACGGTCAGCCAGAACACAGTCGGCAATAAGGTTCCAATTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGAATCCCAATGACTTTGCTTGGAAAAAGACAATGAACACTGCACTGAT
GCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCACCATCCTCGGCTG
CGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAACACTTGGTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCATCCGAGCTGGGCC
ATGGCACCTTGGAGTGTGCTGTGGGCCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGCCACAGC
TTCCCGCTGCACGGGAGAGACGATGCTGATGCCAGGATGACGTGTTCTTATCGTGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAACACCATCATTGGCCACTGTGGACCGAACTGTAACCAAGGGAGAACAGCCCTCACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCAC
TTTTTGAGCAGGCAATCAGCTCTGATTATTGGACTCAGATGTCAGTGTGATCCCCACTCCAACCTGCAGCTCC
ATGTCATAACACCCCTGGCACTGAGAGAGGAAACAGTCGCGCCTCAGTGTGATCCCCACTCCAACCTGCAGCTCC
CAGATGACAGCCCCATCGTAGACGATGACGGATGGCACTGTGGGTGTCGTGATCATAGCCGGTTGCTGT
GTGGTGGGCACGTCACTCGTGTGGTGGTCATCATATACCACACAAGGGAGGAATGAAGATTGCAAGCATTACC
AACACAGATGAGACCAACTGCCAGAGATTCCCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCAAGCTTGTACATCTCAGGTGCTGGATTTCCTACCA
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGAAGCTGCCACAGATCTGTC
CTTTGTCCTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGTATGGCTCAGATCCTTGAACAA
TATCATACAGGTTGCACTGCCAGGAAACAGTTAAATGGACCAACTGAGCCCAGTTACATAAGGAAAAG
GAGTGTACCCATGTTCTCATCTCAGAAAGAATCTGCAAGGAGCTTCAAGTAATATATCGTGGCTTCACAT
GTGAGGAAGCTACTTAAACACTGTTACTCTCACAAATGAGGACCTGGAATGAAAATCTGTCATAACAGTCC
TCTTTAGATTGTCAGGAAATCCAGAGCCAGCGTGGTTGCCAGTAATTCTTACGGTACCTTGAAAGGAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAAGAGCCTT
TTGAAAGCTCATTCTCCCAAGCTTGGACTCTGGTCAAGGGAGATGGGAAAGGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTAACCTTAAACAGACTTAAAGGGAAACTACAGGACTCCAAATTTCAGTCTTATGACTTGG
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACACATACTACCTCAAGTGAACCTTATTAAAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAAGTTATGAAAATTAACTGGGAATGATGTCATATAAGAATACTTTAAACTATTTTAAACTTTG
TTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTGTTATGTTATTAATGCCAGA
TTTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAATACCTGCCCTGTACCAATTAAATAGAAGTT
ACTTCATTATATTGCACTTAAATAAAATGTCATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRI^SAIPPKMFKLPQLQHLELRNPKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEI^LQLDHNNLTEITKGWLYGLLMLQELHLSQNAIRISPDAWEFC
OKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNEIS
WTI^EDMNGAFSGLDKLRRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNACAHQPLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTIIRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKG^EAVLQCIAGGSPPP^EKLNWTKDDSP^ELVTERHF
FAAGNQLLIVDSDVSDAGKYTC^EMSNTL^EGNVRLSVIPTPTCDSPQMTAPS^EDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGT^EAD^EQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATD^EFLCPFLG^ESTGPMY
LKG^ENVYGS^EDPFETYHTGCSPD^ERTVLM^EHYEPSYIKK^ECP^ECSHPSE^ESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDF^EANPEPASVASSNSFMGTFGKALRRPHLD^EAYS
SFGQPSDCQ^EPRAFYLKAHSSPD^ELSGSEEDGKERTDFQEE^EHNICTFKQ^ET^ENYRTPNFQSYDLD^ET

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAACCTTGCCTGGAGAGCGCCCCAGCTTGAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGGAGCGCTTGGCCTGCCCCGCTCGGCCGGGCGAGCAGGGAAAGGGGAAGCTGTGGTCTGCC
CTGCTCACGAGGCCACTGGTGTGAAACCGGGAGAGCCCCCTGGTGTCCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGAAAGGCAGCGCAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAATGGAAAGGCAGGGCAGAACAGCCTGCC
TCCATCAGCCCTGGGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGTGTGC
TGCTCTGCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCCTGAGGGCCCCAGGATTGGCGAA
GTGGCGCCACAGCCTGAGCCCCGAAGAGAACGAATTGGAGGGAGGAGGCCGGTGTGACTGAGCCTGAGG
AGCCCGGGCTGGCCAGCCGGTCACTGCCCCGGAGACTGTGCTTCCAGGGGGCTGTGACTGTG
GCGGTATTGAGCTGGTGAAGTCCCCGGGGACCTGCCTGAGCACACCAACCTATCTCTGCAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCCCGGCTGACCGGACTGGAGACACTGAACACTGCAAACACCCTGA
CTTCCCAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGACTTGGCAATAAACAGC
TGACCTTGGCACCCGCTTCTGCCAACGCCCTGATCAGTGTGACTTGTGCTGCCACTATCTACCAAGATCT
ATGGGCTCACCTTGGCAGAACGCAAACCTGAGGTCTGTGACTCTGCACAAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCTGCTCCAGCAACTCCTGCGCACGTGC
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCCT
TCAGCGAGCTGAGCAGCCTGGCGAGCTAACCTGAGAACAAACTACCTGACTGACGAGGGCCTGGACAAACGAGA
CTTCTGGAAGCTCCAGCTGGAGTACCTGGATCTGTCCAGCAACAAACCTGTCTGGTCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGTCAGCAACAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTCCAGGGCC
TCAAGCGGTTGACACGGTCACCTGTACAACAAACGCGCTGGAGCGCGTGGCCAGTGGCCTGCTGCCCGTGC
GCACCCATGATCTGACAAACAGATCACAGGATTGGCCGAAGACTTGGCACCAACCTACTTCTGGAGG
AGCTCAACCTCAGTACAACCGCATCACAGGATTGGCCGAAGACTTGGCACCAACCTACTTCTGGAGG
GCTCGCTGGACCTGCTGGCAACCGGCTGACACGCTGCCACCTGGCTGCAATGTCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCTTGGCACAGGGGGCCTGGCGGAGTGGCTCAGCTGCTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCGAGCCCTGGGCCCCGTGCTGGTGGACCTGCCATCTCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACCTGAGTACCTGACAGAACAAACA
AGATTAGTGCCTGGCCCAATGCCTCGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGAGGCTTGGACATTGAAGGCAACT
TAGAGTTGGTACATTCCAAGGACCGTGGCCCTGGGGAGGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAAGATGTGACCTAGGATGATGGACGCCGGACTTTTCTGC
AGCACACGCCCTGTTGCTGACTGCCACAGCCCCACTCTGCCGTGTCACACAGACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTGCCAGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCCCTAAACACCCAGCTCAGCCACACACAACCTACCCCTCAAACCCACAGTCTCTGTCACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAAGGGCTGCCCTGCCAGCAGGCCACACAGGCCACCA
TCCCTCCCCCTGCTGACATGTGCTGATGCAACACACACACACAGCAGCTGACAGCTGCTGCCCT
CAGCCCTCAAAGCTATGCCACAGACAGCTTGCCTGGCAGAATCAGGAGTGGCTGCTGCCAGGGCTTCT
GTCCATCTGCTGGCTCCGGTGTGGAGAAGACACAAAGGGTATCCATGCTGTGGCAGGTGCTGCCACCCCT
GGAACCTACAAAAGCTGGTTTATTCTTCCCATCCTATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
TGGCCACCCCTGCTCCAGGTGCTGGCAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTCAATGGGAAGGCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GTTCTCAGGCCCTGTGGGGAGGTTCCGGTGCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAAAT
CTAAAGCTGATTCTTCTGTTAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPVLVLSPEEPGPGPAAVSCP RD CACS QEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNQNNRLTSRGLPEKA FEHLTNLYLANNK
LTLAPRFLPNALISVDFAANYLT KIYGLTFQKPNLRSVY LHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVD SAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVQCQPRCKHGE
CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDG
GSCSSALTCSMANCQYGCDDVVKGQIRCQCPSPGLHLAPDGR
TCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIIGGKYQCHDIDECSLGQYQC
SSFARCYNVRGSYKCKCKEGYQGDGLTCVYIPKVMIEPSGPIHVPKG
NGTILKGDTGNNNWPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLP
PTPERPTGLTTIAPA
ASTPPGGITVDN
RVQTDPQKPRGDVF
SVLVHSCNF
DHGLCGWIREK
DNDLHWE
PIRDPAGGQYLT
VSAAKAPGG
KAARLVLPLG
RLMHSGD
LCLSFRH
KVTGLHSG
TLQVF
VRKHGA
HGAALW
GRNGGH
WRQTQI
TLRGADIK
SEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGCTGA
AGGTGACAGTGCCATCACACACTGCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAAGTTCACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACCTATCTGCCAGTCA
GAAGATAACAAGTCACGGTGTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAATGGAGACCTGTCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGAGGAACCCTGTCACTGAAATGGAAAGTGTATCATATTGCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGCTAAAAGTAGGGAAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTTCTCTTCTATGGAAAAAAATATCAACCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAG**TGA**ACTTCTATGG
GCTAAACAGTACATTGAGTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTTACTCATTATTCTTACA
TGCAGAACAGGCAATTGAACTGCAACTGCAAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGCAATTGTTCAATTAAATTCTATCTGTTATTGTACAA
TTAAGAATGCTAAATTATGTTCAATTAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTGTCAAAAAACAAAATGCTCTCTTCAATCACC
AGTAGTATTGGAGAGACTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTTGCTTTAAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNVKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ
KIQVTVDVPVTKPVQIHPPSGAVEYVGNMLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMVDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTGCAGTCCCTGGCAGTCCTGGTGCTGTT
GCTTGGGGTGCTCCCTGGACGCACGGCGCGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGCTGAATGGGGAGAAGATCTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTCAGTGGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT
TATTATCAGAACATCTGCACAAACCTTGAAAAAAAGTGGAGGAGGAACAAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC
CATAAAGACAAACGCTCTGGTCCATCATTGCCACAGATAAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTGATAAAACAGAACAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAGGGTTCAAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTAGAACATAAAAGCACTAGGTATACAAGTTGAAATTGATTAGCACAGTATGATG
GTTAAATAGTTCTCTAATTGAAATCGTGCAGCAAGCAATAAGATTATGATATTGATATTGT
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCAGTATTGATT
TGAGGTATTAAAGAAGATTATTAGAGAAAAATTCTCATTTGATAATAATTCTCTG
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCAGTGACAATTCTGTTCTTACTATGGGTTACATTATTATT
ATTAGGTTATGCAACTAAACAAACTACCTTACATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCACTGGTATTCTCTGATT
CAACAAAGTTGATTCTTCTGTATTCTTACTTACTATGGGTTACATTATTATT
CAAATTGGATGATAATTCTTGAAACATTTTATGTTAGTAAACAGTATTGTT
GTTCAAACGTAAAGTTACTGAGAGATCCATCAAATTGAAACAATCTGTTGAATTAAATT
TTGCCACTTTTCAGATTACATCATTCTGCTGAACCTCAACTGAAATTGTTTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTGTTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAAATTCAAAGAACGTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG
CATCTCTGTATATGCTTAAATGTATTGTCCTCATATACAGAAAGTTCTTAATTGAT
TTACAGTCTGTAATGCTGATGTTAAATAAACATTATTATTTAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATATTGTTGTTGAACTTCACAGGAAAA
GTCAGTAGGATGGAACATTAGTGTATTCTACTCCTTAAAGAGCTAGAACATAGTTT
CACCTTAAAGAAGGGGGAAATCATAAAATACAATGAATCAACTGACCAATTACGTAGAC
AATTCTGTAATGCCCCCTCTTCTAGGCTCTGTTGCTGTGAAATCCATTAGATTACAG
TATCGTAATATAACAGTTCTTAAAGCCCTCTCTTAAAGGTTGAAATTAAATATTGACCATT
AAAGAGTTGGATGTGTAACCTGATGCCTTAGAAAATACCTAACGACAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCAGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATGAA**ACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGCCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAAGAGCTGGGCAACAAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCAGGAGCTTCTCCCACGTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTTCCAGTGGGTGATCTGCACCGTGCCTGGAGGCTCACCGCCGCTGCTC
TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGAAATCTCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCCTGGAACACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCTGGG
GAGGGTGTCAAACGTACACCCCCGTAGACAGAAGAGGGCTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTCATTCGCCCCCTCAAAGAGGAGGACGAGTGGGACAGCCGACA
TCGTCAGGTACTACGATGTCATGTTGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACGCCACCGTTGATCCCAAGACAGGAGTCCCACTGTGCCAGCTA
CCGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCAAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTGTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGTAAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACT**GA**CATCCTTTCTGTCCTTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTAGCAGGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCACTGAAACAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCCTACCAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTKSQVLQDLSYAVFQLGDLHRAELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIYRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTGGCTGGGGTTAGTTCGACACCTTCACAGTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGCCTGGAAGCCAGGGGCTTGCTCTGCTCTGCTTTGGCCTATTGACCC
CAGGTTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGCCTCAATCATTGATCCTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGCTCTGGGTGAGCCTGAGCCTGCGGGTTCCCTGGATCCAGGGGAGGGAGAAG
ATCCCCTGTGAGGGCTGTAGGGGAGCGAGGAGGGCACAGAACATCCAGATTCGAGAGCTGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCGGATGTCCTACTACAGGGACCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTGCTGGGCTGTGACCTCCGAGCTACACTGTCCA
CTTTGGCGTGGCTGTGAACCGTACGGTGCCCCATCACTCCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGGTGGTGTCTCATGGGATGAGCGGCCCTGGCTCATGTAGAGACCCCTGC
GCCACCTTCACACACACTTGGGCCGACTACGACTGGTTCTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCGCCTGGCAGGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTATTG
GCGCAGGGCAGCAGGGCCGGTACTGTATGGGGCTTGCTACCTGTTGTCACGGAGTCTCCGTGCTGC
GCCACATCTGGATGGCTGCCAGGAGACATTCTCAGTGGCCCTGACCGAGTGGCTGGACCGCTGCCATTG
ACTCTCTGGCGCTGTGCTCACAGCACCCAGGGCAGCAGTATCGTCATTGAAACTGGCCAAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCCGTGACCCCTGCTCGGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTTGGAGCTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGAGGCAGGGCTGAGCTGGCCCTGGCTCCCTGCTCCTTCA
CACACACACTCGCTTGAGGTGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTGAGATGGGG
CTCCCAAGTGCCCACACAGGGGCTAGCAGGGCAGCTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTTCAAGCAGCGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTTGGAAATGTGTGACACAGCGTGGGCACCCGGGGCTGGCTCGCA
GGGTCACTGCTGCCACTGAGCGGGTGGAAATCCTACCTATGCCATGTCACTGAGGCCACCCAGTGC
AGCTGGTGTGCCACTCTGGCTGAAGCTGCTGCAGCCCCGGCTTCTCGAGGCCTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGGAGCTCCAG
ACCCATTCTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCCTGGAGCAGGCTGGCTGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAACCCCTGAGGACACTCT
TCTTCTTACCAACCGTGTGGACAAGGCCCTGGGGCCGAAGTCTCAACCGCTGTGCAATGCCATCTGGCT
GGCAGGCCCTCTTCCAGTCCATTCCAGGAGTTCAACTCTGCCCTGTCAACAGAGATCACCCCAAGGCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTCTGGAGGGCTGCTTACAACGCTGACTACCTGGCCCGAGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCTCCGGTTCTCAGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGTGCCTGCCTCAGCAACCTGGAGGGCTAGGGGGCGTGGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTAGCCCTGGCCCTGGGGCCCTAACCTATTACCTTGTCTGCCCTAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSILGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVDALETALEQLNRRYQPRLRFQKQRLNGYR
RFDPARGMETLDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL
VAEAAAAPAFLEAFAANVLEPREHALLTLVVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTVWTRPGPEVLRNCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGCAGGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTCAGTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTTGACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTACAGCCTCT
CAATATCCCAGAAAAGTGCCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTGTTCAAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACGCCTTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGAGTAGTAACTACATATCCAA
TACAGCTGTATGTTCTTTCTTCAATTGGTGGCAGTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAAAACTATTAATAAAATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAGTAAAACCTTAGCTGTGTTCCCTTACTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCCTCTCAAAATGTACAACAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPKEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCCACCGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAGAAAGAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACCAGATGTGTTGTGACATTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCACTGAGAATTTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCACTGAGAATTGTTGCCATTGAACGGAAATATTTCAATCC
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTCAACAGA
AACCTAAAATGAGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGAGCCAAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTCTTTAAGACAGAAGGCACAACCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATAACAAATAAAATAAGTAGTTAAATGTTAAAAA
AAAAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDTSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCGACTTCTTCTGCTGCTTTCAGGGGCTGCCGATAGGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGAACTGTCTTGATCATTACGGATTCGC
AGACAAGTGACCCAGGATCGAGTGGAAAGAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGGGGCTGTCAGAAATACTGGGAAGACATCCCTGAAGATCTGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGCTGCGAAATGACCGAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTCTTCACTTAAACACTGAAACAGGCACCTTGGTGTACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGGTCTGTTGTCCTGCTGACTGCCCTGA
TCACGTTGGCATCTGCTGTGACATACAGACGTGGTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACATCCGCACTGACGAGGGAGGGCGACTTCAGACACAAGTCATGTTG
TGATCTGAGACCCGGGTGAGGGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTGAGAAACTCCTGTC
GGCAGCGAGAGCTGATGCACTGGCACAGAGCTAGACACTCATTCAGAAGCTTTCGTTGGCCAAGTTGACCA
CTACTCTTCTACTCTAACAAAGCCACATGAATAGAAGAAATTCTCAAGATGGACCCGGTAAATATAACCA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTCTGGCTGATTCGGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCGTGCTGGGCTGTGAAGCCAGCATGTTCACCACTGGTC
CAGCAGCCACGACAGCACCAGTGAGATGGCAGGGGGCTGGACAGCACAGCAGCGCATCCGGCGGGAACCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGGCCACAGACACCACCGCAGTTCTTCTTAAAGGCTCTG
TGATCGGTGTTGCAGTGTCCATTGAGGAGGCTTTGGATCAGCATTGTAAGGAAACACAAACAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGGCTGAGGAACCCCTGTTGCTAACAGGGTGTAGGATTTAAGGAA
ACCTTCGTCTTAGGCTAACAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTAAAGGAA
TACATCTAAATTGGCTAACAGGATGTTGATTGATTGAAAGAAATTCTATTTAAACTGTAATATATTGT
CATACATGTTAAATAACCTATTAAAGTCAACTTAAGGTAGAAGTCTAACAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTACCAAGGAATCCTCTCATGGAAAGTTACTGTGATGTTCTTCT
CACACAAGTTTACGCTTTTACAAGGGAACTCATACTGTCACACATCAGACCATAGTGCTTAGGAAACCTT
TAAAATTCAGTTAACAGTGAATGGTAAAGTCTGAAATCAGTTGATCTCTCAAAAGAAACCTCAGGTAGCTTGA
ACTGCCTCTCTGAGATGACTAGGACAGTCTGACCCAGAGGCCACCCAGAAGCCCTCAGATGACATACAGATG
CCAGTCAGCTCTGGGTTGCCAGGGCCCCGCTAGCTACTGTTGCTCGCTGTGCTGCCAGGAGGCC
GCCATCCTGGCCCTGGCAGTGGCTGTGCTTCACTCAGTGGCCCTGCTTCACTCCAGCAGC
TCTCAGGGGGACTGCAGGGACACTGGGTCTTCACTGAGCTCCAGTGGCTCTGTTAAGGCTCTGTA
TCTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTTAAGTTGTTAATTATTGTT
AAGATTGCTAACGGCCAAGGCATTGCGAAATCAAGTCTGTCAAGTACAATAACATTAAAGAAAATGGAT
CCCACTGTCCTCTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAACATTGACTTTAACATTTCATCCGGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCAGTCCACTGTTGCTGCC
GAATGGCTCTCAACTCACCCTGTCTTCACTGCTTCAAGTGTCTGGTTTTTAAACTTTGACAGCTTTTTT
AATTGCTACATGAGACTGTGACTTTTTAGTTAGTATGAAACACTTGGCGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTCTGCTGCTGATGGCATCTGGATGCTTAGCATGCAAGTT
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCACCCCTCAGCCTGGGATTCACTGCTCCAGCCT
TCTTGGTTGTCAGTGTAGGGTAGCCTTATTGCCCTTACCCCTAACCTTCAACTAGTGC
TGGGAACCAAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCCTTGGATGGATGTTGCTGACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSKIKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIGG
VLVVLAVLALITLGIICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267